

Figure 1

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
TAAAGGTAAATAGAACTGCATTTCCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179
Identities = 319/319 (100%)
Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 60
|||||
Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 120
|||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgaa 180
|||||
Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgaa 834

Query: 181 aatcagcctaaaggtaaataagaaactgcatttcccctccattcttgaagccaatctttt 240
|||||
Sbjct: 833 aatcagcctaaaggtaaataagaaactgcatttcccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 300
|||||
Sbjct: 773 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319
|||||
Sbjct: 713 caagctttggtacaggatc 695

Figure 2

cDNA Sequence and ORF of 85P1B3/OIP5 clone A

5'	9					18			27			36			45			54	
	GGC	TGC	GGG	AAG	ATG	GCG	GCT	CAG	CCG	CTG	CGG	CAT	CGC	TCA	CGT	TGT	GCA	ACG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
				M		A	A	Q	P	L	R	H	R	S	R	C	A	T	
	63					72			81			90			99			108	
	CCG	CCC	CGG	GGG	GAC	TTT	TGT	GGT	GGC	ACT	GAG	AGG	GCG	ATT	GAC	CAA	GCT	TCT	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	P	P	R	G	D	F	C	G	G	T	E	R	A	I	D	Q	A	S	
	117					126			135			144			153			162	
	TTT	ACG	ACC	TCC	ATG	GAG	TGG	GAT	ACG	CAG	GTG	GTG	AAG	GGG	TCC	TCG	CCG	CTC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	F	T	T	S	M	E	W	D	T	Q	V	V	K	G	S	S	P	L	
	171					180			189			198			207			216	
	GGC	CCC	GCA	GGG	CTG	GGG	GCT	GAG	GAG	CCA	GCC	GCC	GGC	CCG	CAG	CTG	CCG	TCT	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	G	P	A	G	L	G	A	E	E	P	A	A	G	P	Q	L	P	S	
	225					234			243			252			261			270	
	TGG	CTG	CAG	CCT	GAG	AGG	TGC	GCT	GTG	TTC	CAG	TGC	GCA	CAG	TGT	CAC	GCA	GTG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	W	L	Q	P	E	R	C	A	V	F	Q	C	A	Q	C	H	A	V	
	279					288			297			306			315			324	
	CTC	GCC	GAC	TCG	GTG	CAC	CTC	GCC	TGG	GAC	CTG	TCG	CGG	TCC	CTC	GGG	GCC	GTG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	L	A	D	S	V	H	L	A	W	D	L	S	R	S	L	G	A	V	
	333					342			351			360			369			378	
	GTC	TTC	TCC	AGA	GTT	ACA	AAT	AAC	GTC	GTT	TTG	GAA	GCG	CCC	TTC	CTA	GTT	GGC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	V	F	S	R	V	T	N	N	V	V	L	E	A	P	F	L	V	G	
	387					396			405			414			423			432	
	ATT	GAA	GGT	TCA	CTC	AAA	GGC	AGT	ACT	TAC	AAC	CTT	TTA	TTC	TGT	GGT	TCT	TGT	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	I	E	G	S	L	K	G	S	T	Y	N	L	L	F	C	G	S	C	
	441					450			459			468			477			486	
	GGG	ATT	CCC	GTT	GGT	TTC	CAT	CTG	TAT	TCT	ACC	CAT	GCT	GCC	CTG	GCT	GCC	TTG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	G	I	P	V	G	F	H	L	Y	S	T	H	A	A	L	A	A	L	
	495					504			513			522			531			540	
	AGA	GGT	CAC	TTC	TGC	CTT	TCC	AGT	GAC	AAA	ATG	GTG	TGC	TAT	CTC	TTA	AAA	ACA	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	R	G	H	F	C	L	S	S	D	K	M	V	C	Y	L	L	K	T	
	549					558			567			576			585			594	
	AAA	GCC	ATA	GTA	AAT	GCA	TCA	GAG	ATG	GAT	ATT	CAA	AAT	GTT	CCT	CTA	TCA	GAA	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	K	A	I	V	N	A	S	E	M	D	I	Q	N	V	P	L	S	E	
	603					612			621			630			639			648	
	AAG	ATT	GCA	GAG	CTG	AAA	GAG	AAG	ATA	GTG	CTA	ACG	CAC	AAT	CGC	TTA	AAA	TCA	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	K	I	A	E	L	K	E	K	I	V	L	T	H	N	R	L	K	S	

		657			666			675			684			693			702
CTA	ATG	AAG	ATT	CTG	AGT	GAA	GTG	ACT	CCT	GAC	CAG	TCC	AAG	CCA	GAA	AAC	TGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	M	K	I	L	S	E	V	T	P	D	Q	S	K	P	E	N	*
		711			720			729			738			747			756
TCC	TGT	ACC	AAA	GCT	TGA	GTG	TCA	GGT	TCA	GGC	TTT	ATT	GCT	GTC	TTC	AAC	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		765			774			783			792			801			810
AGG	TGC	TGC	TTA	GTC	ATT	TCT	TGA	AAA	AGA	TTG	GCT	TCA	AGA	ATG	GAG	GGG	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		819			828			837			846			855			864
TGC	AGT	TTC	TAT	TTA	CCT	TTA	GGC	TGA	TTT	TCC	AAA	TTA	TTT	GTG	AAG	CTG	TTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		873			882			891			900			909			918
TTA	GAA	GAT	GAG	AGA	CTA	AGG	ATT	CTT	CTC	TTT	TAT	AGC	TAT	TTG	CCT	TAA	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		927			936			945			954			963			972
CTT	ACT	TTA	GAT	TCT	TAT	TGA	ATT	CAT	AAT	ACT	TAT	CTC	TGA	AAA	TGT	CTT	TGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		981			990			999			1008			1017			1026
CTG	TAA	ATT	TAG	GAA	TTA	AGA	TGC	AGA	GTC	CCA	TGT	GTC	CTC	TGA	TCT	AAA	GTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		1035			1044			1053			1062			1071			1080
GCA	TGG	TTG	GTC	TGA	AAA	TAG	AGT	TGG	GCT	TAA	TGT	TGA	CTT	CTA	TTA	CTC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		1089			1098			1107			1116			1125			1134
CAT	GGA	GCA	GTT	GTT	ATG	AAT	ACT	AAT	ACA	TCA	CTT	TTT	AAC	TTC	TGT	AAA	ATA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		1143			1152			1161			1170			1179			1188
CAG	ATC	ATA	ATA	TTC	TAT	AGG	TAA	TGT	TTA	ATA	AAT	TGC	CTG	AAT	AAT	AAA	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		1197			1206			1215			1224			1233			1242
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		1251			1260												
AAA	AAA	AAA	AAA	AAA	AAA	AA	3'										
---	---	---	---	---	---	---	---										

Figure 3

85P1B3/OIP5 protein sequence.

```
1  MAAQPLRHRS  RCATPPRGDF  CGGTERAIDQ  ASFTTSMEDW  TQVVKGSSPL  GPAGLGAEPP
61  AAGPQLPSWL  QPERCAVFQC  AQCHAVLADS  VHLAWDLSRS  LGAVVFSRVT  NNVVLEAPFL
121 VGIEGSLKGS  TYNLLFCGSC  GIPVGFHLYS  THAALAALRG  HFCLSSDKMV  CYLLKTKAIV
181 NASEMDIQNV  PLSEKIAELK  EKIVLTHNRL  KSLMKILSEV  TPDQSKPEN*
```

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

```
85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSM EWDTQVVKGSSPLGPAGLGAE EP 60
      MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSM EWDTQVVKGSSPLGPAGLGAE EP
OIP5: 3  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSM EWDTQVVKGSSPLGPAGLGAE EP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRV TNNVVLEAPFL 120
      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRV TNNVVLEAPFL
OIP5: 63  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRV TNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV 180
      VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV 182

85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
      NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231
```

Figure 5: 85P1B3 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

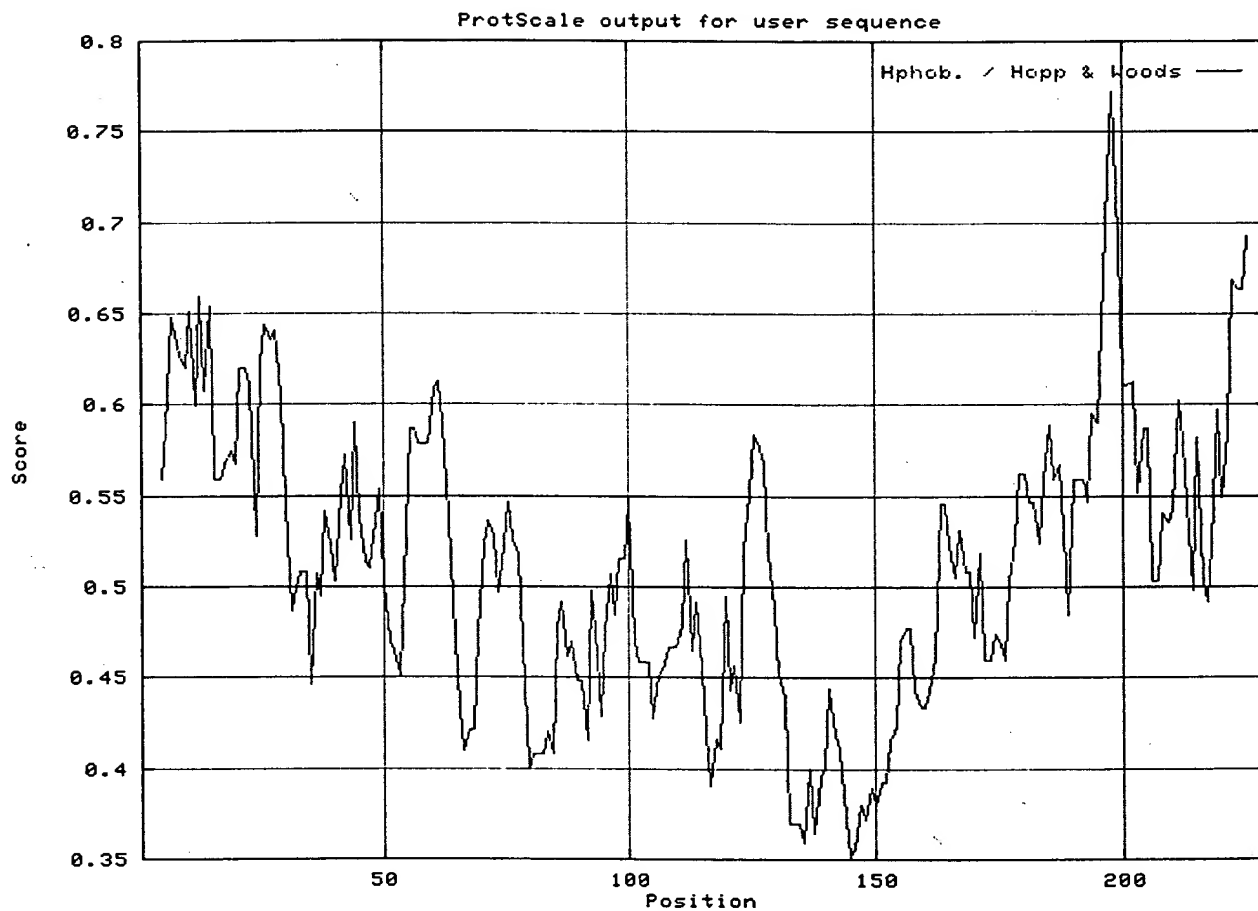


Figure 6: 85P1B3 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

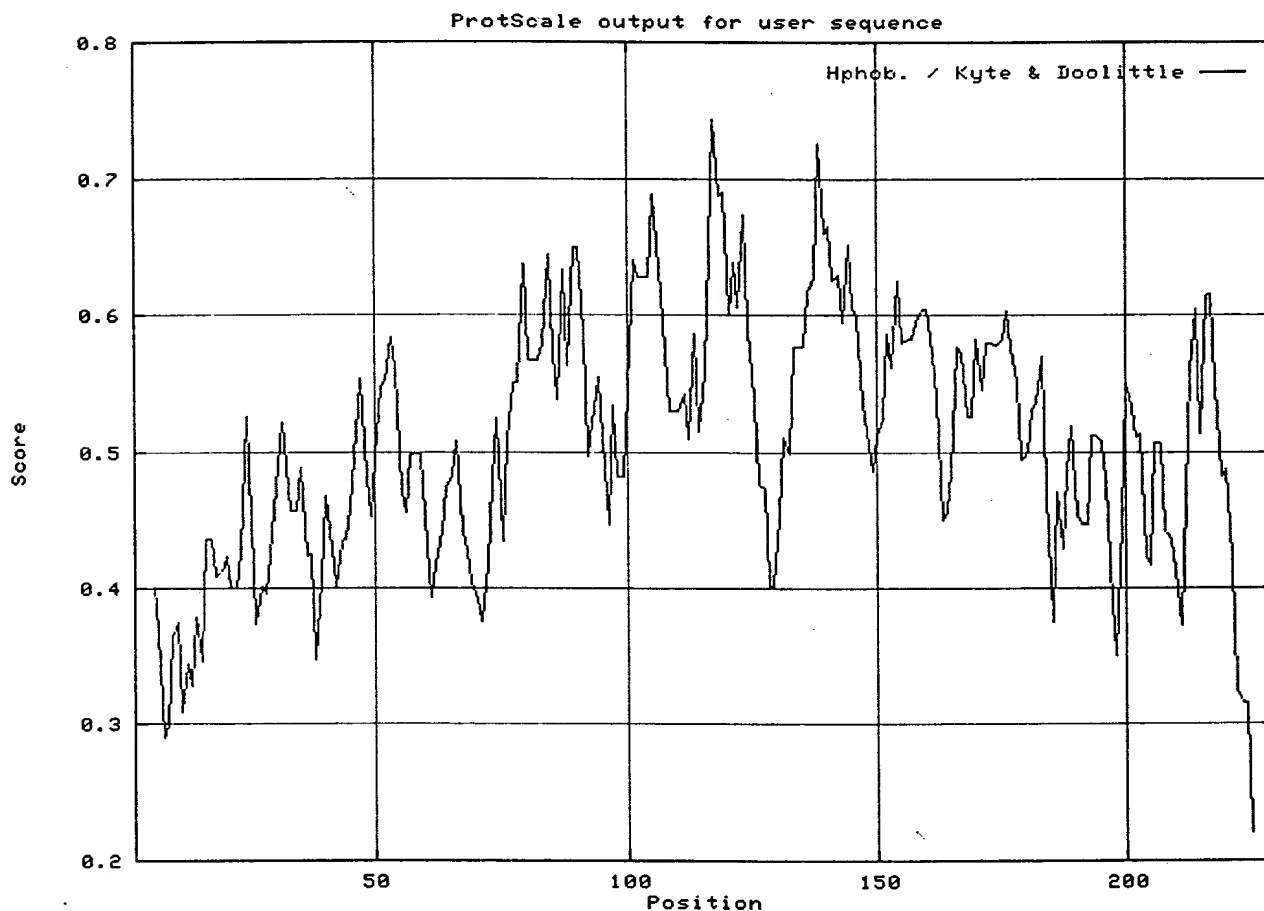


Figure 7: 85P1B3 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

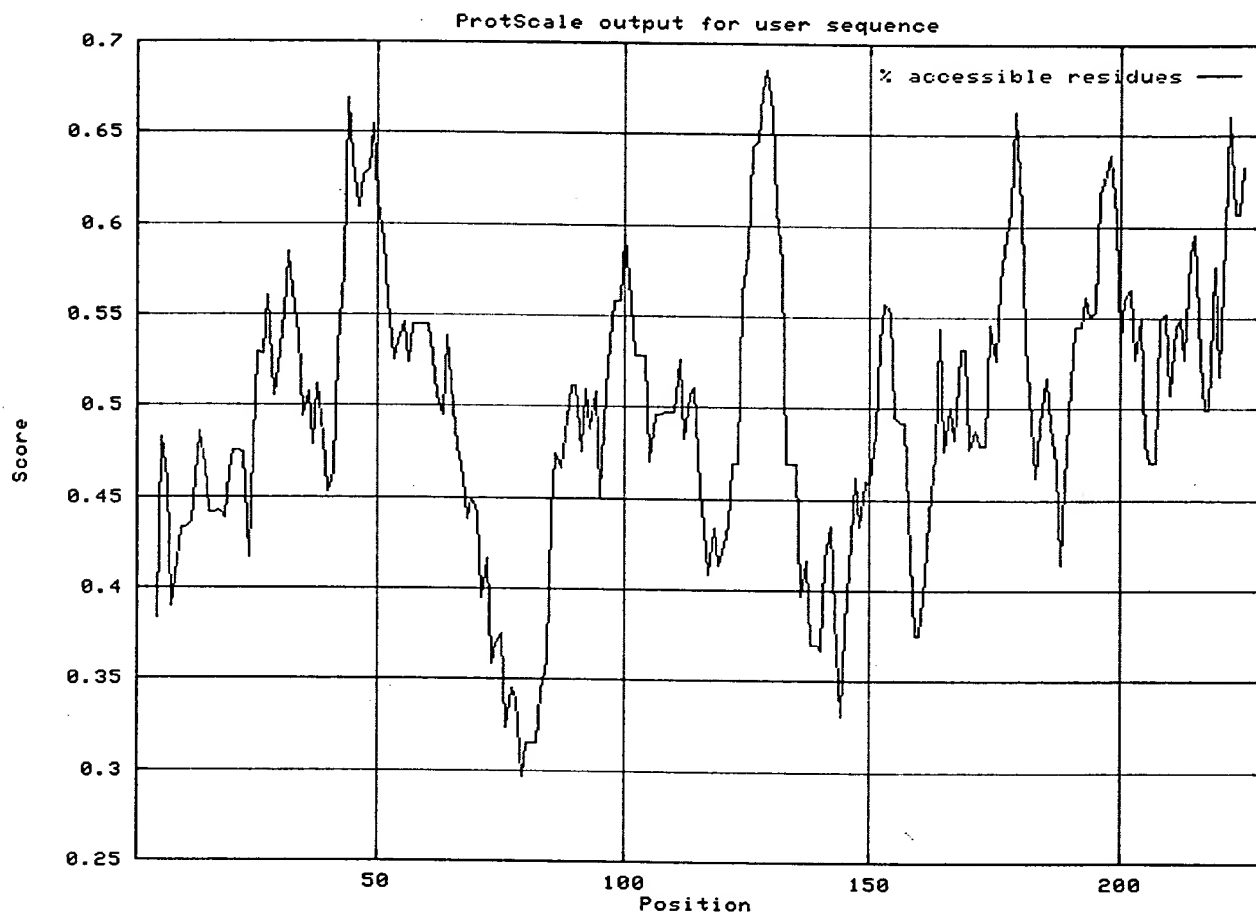


Figure 8: 85P1B3 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

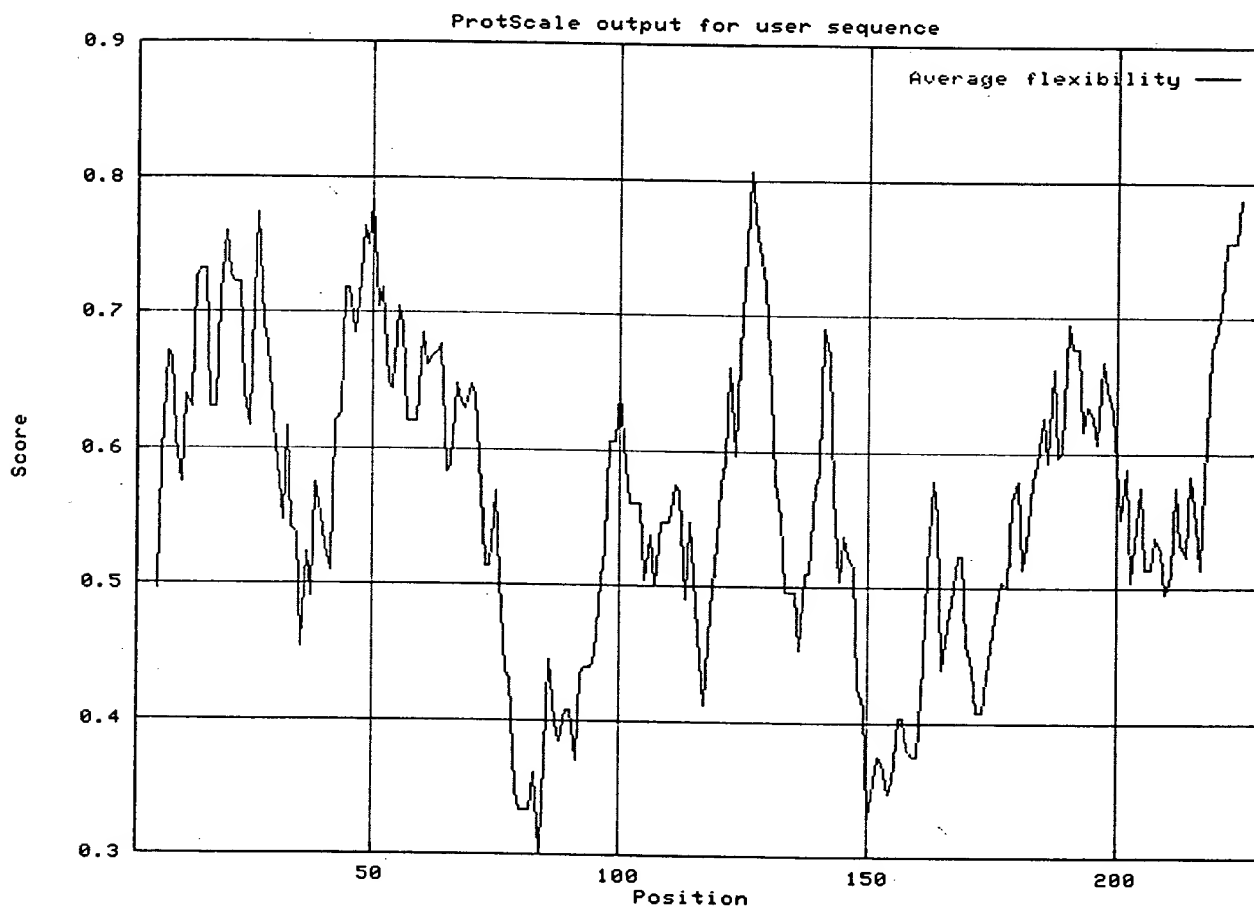


Figure 9: 85P1B3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

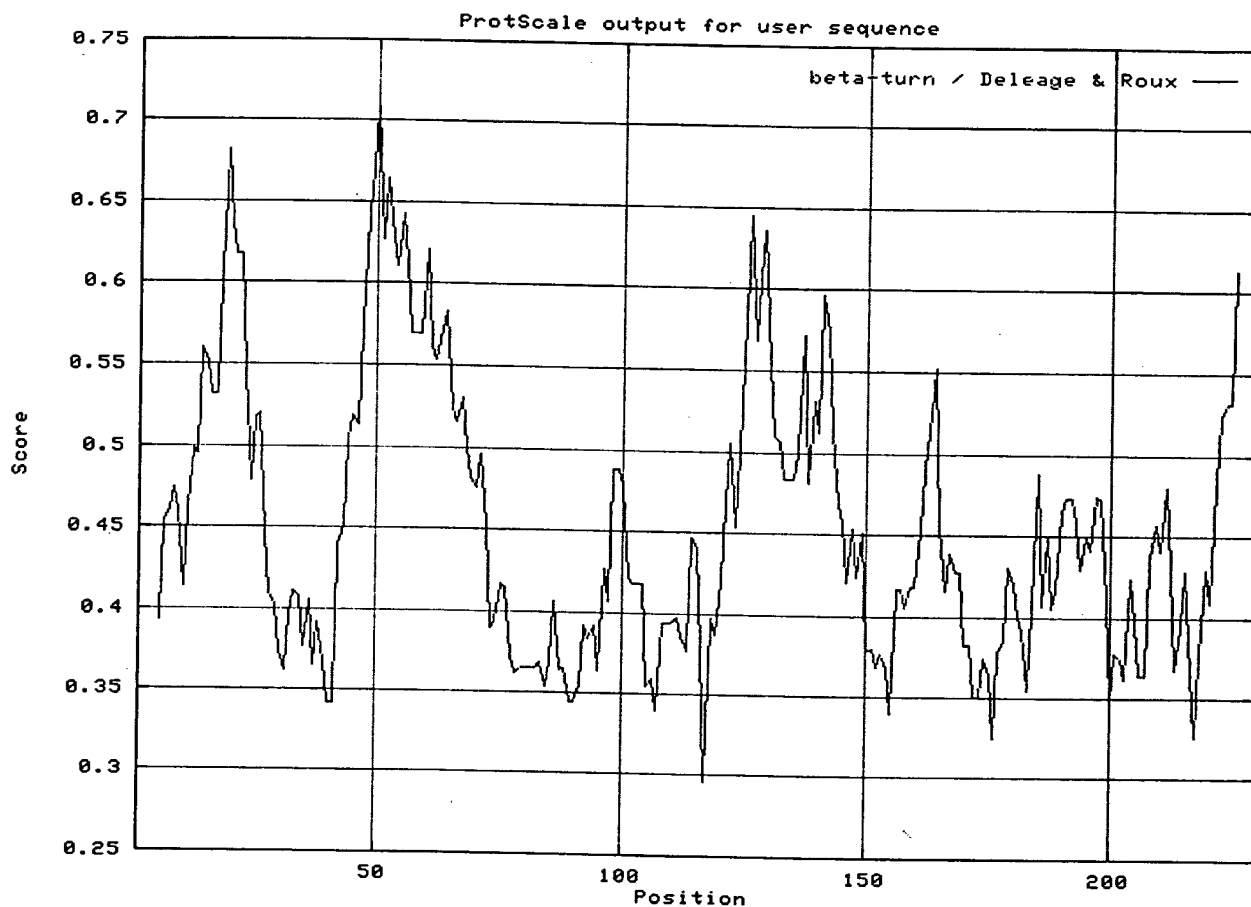


Figure 10 RT-PCR analysis of 85P1B3 expression.

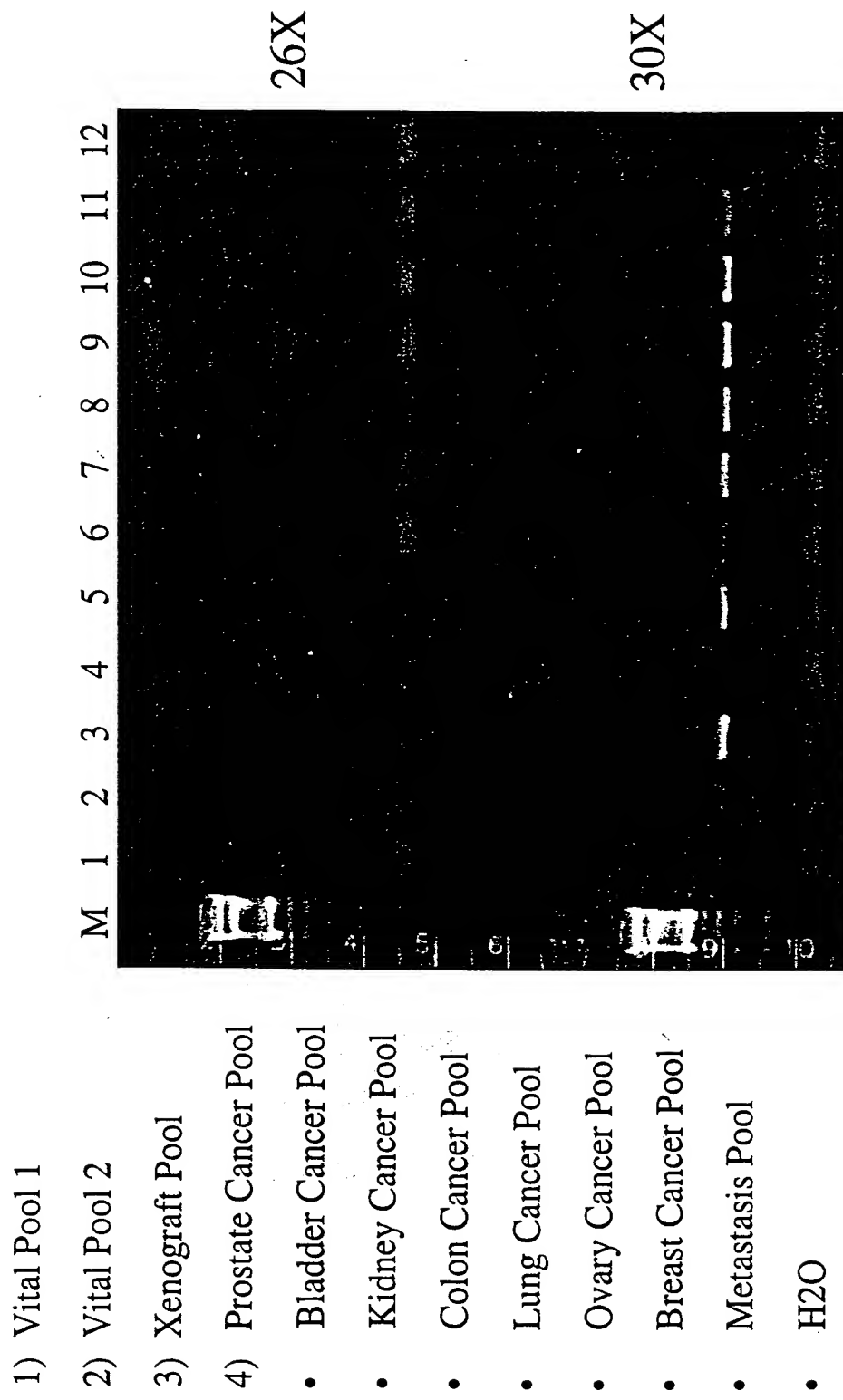


Figure 11 Expression of 85P1B3 in Normal Human Tissues

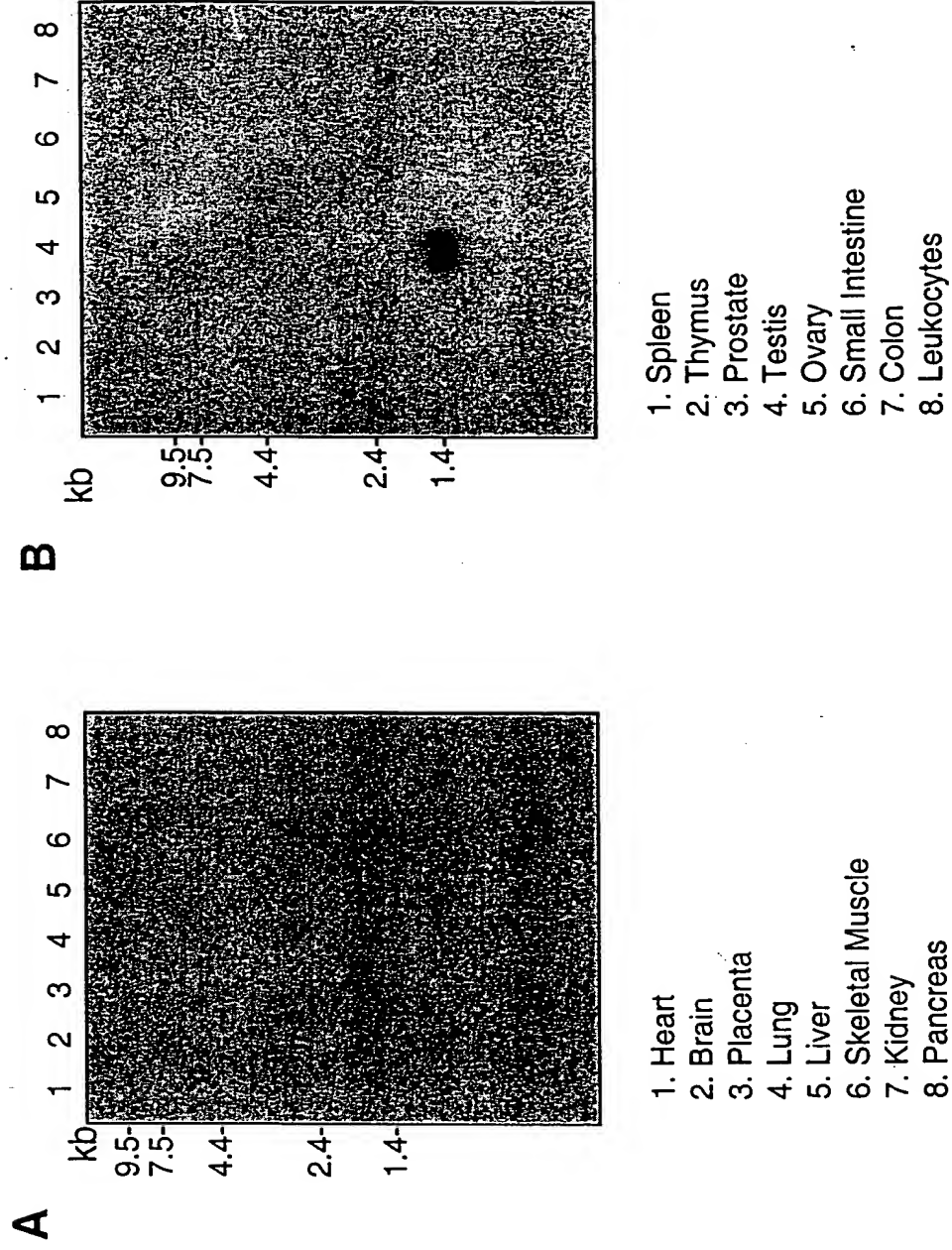
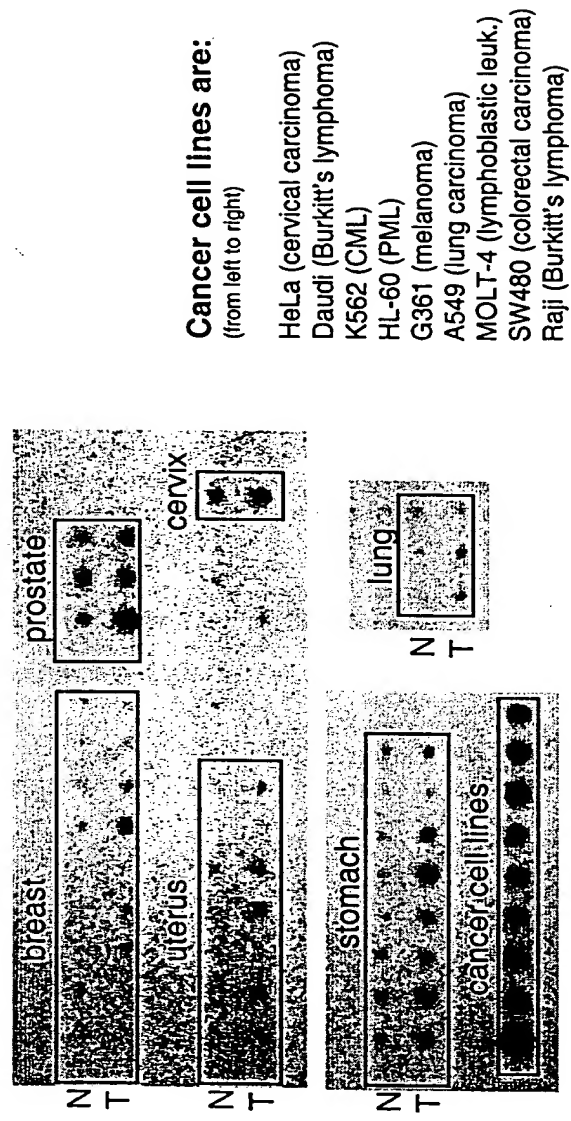


Figure 13 Expression of 85P1B3 in Patient Cancer Specimens and Cancer Cell Lines



T = tumor RNA
 N = normal adjacent tissue RNA

Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens

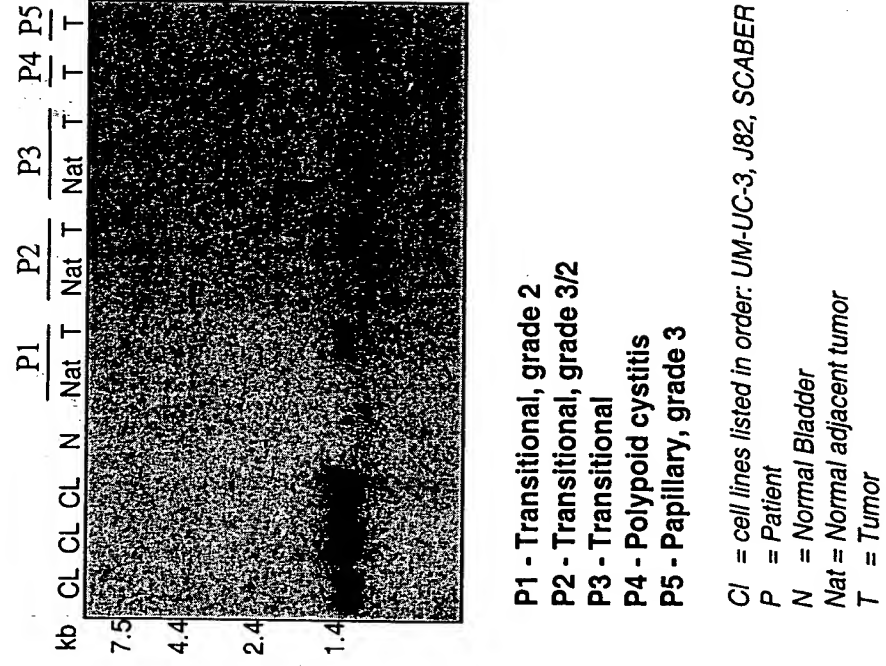
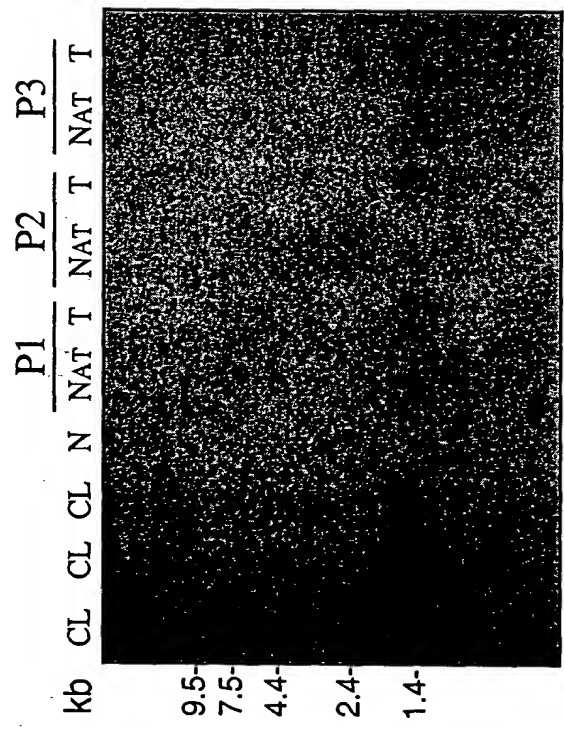


Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens



P1 - Squamous, stage IB
P2 - Squamous, stage IIB
P3 - Squamous, stage IIIA

CL = cell lines (listed in order):
A427, NCI-H82, NCI-H146
P = Patient
N = Normal Lung
NAT = Normal adjacent tissue
T = Tumor

**Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following
Castration**

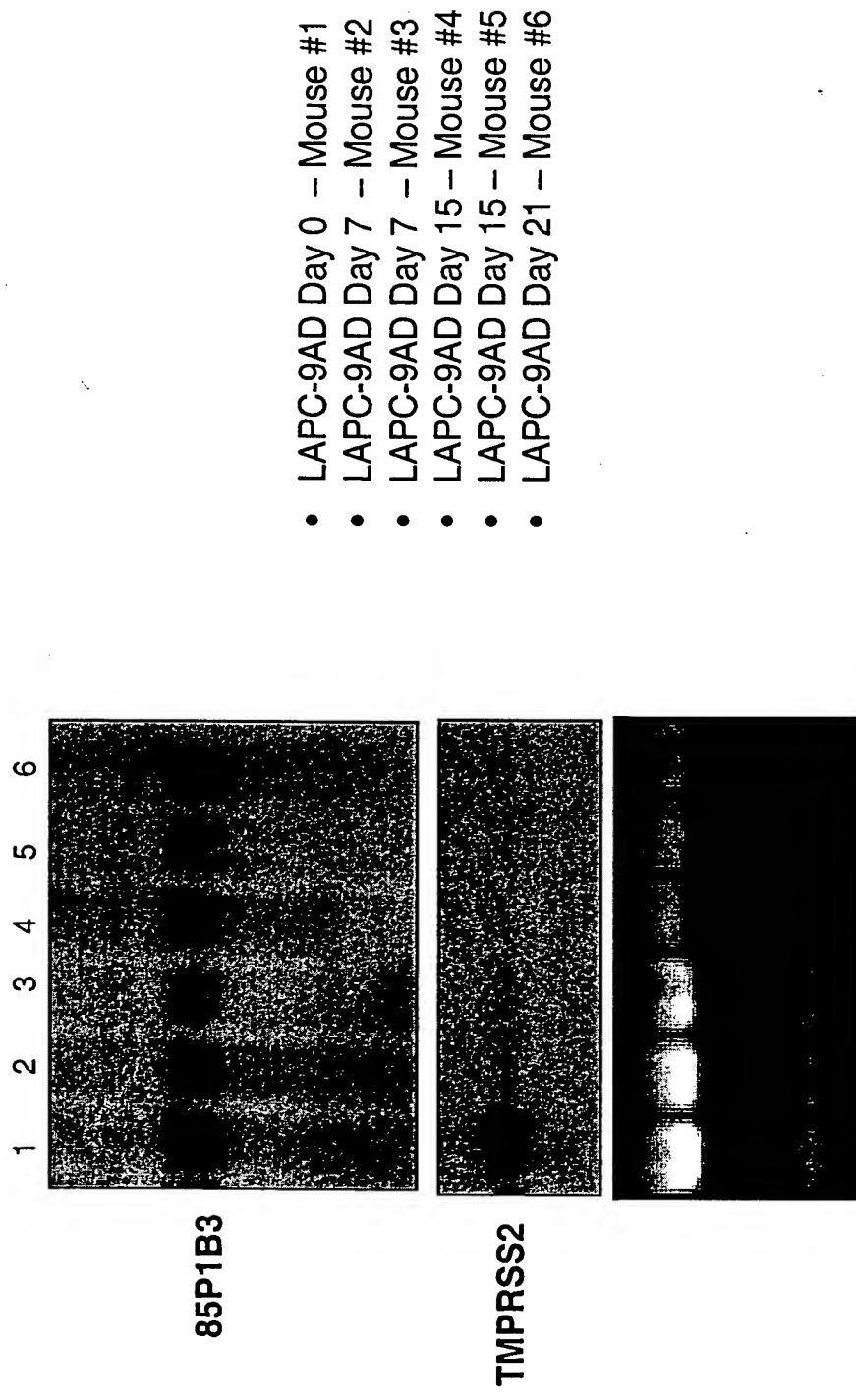


Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery

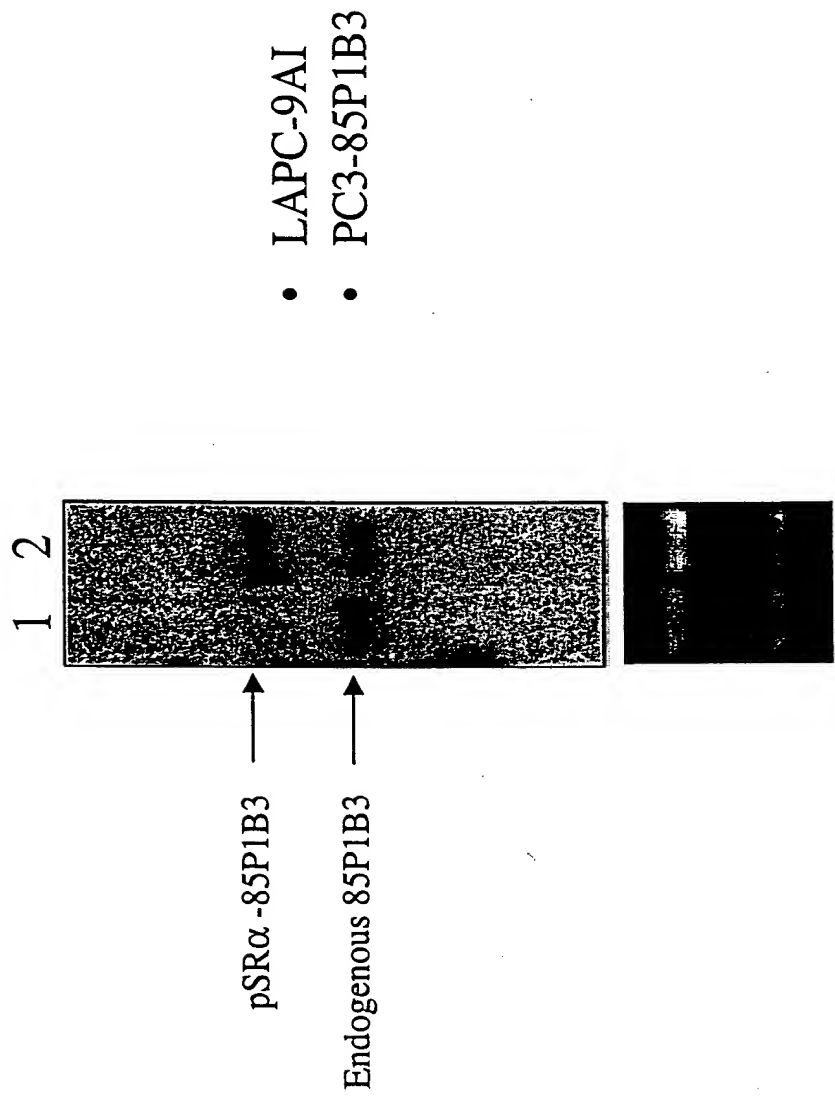


Figure 19.

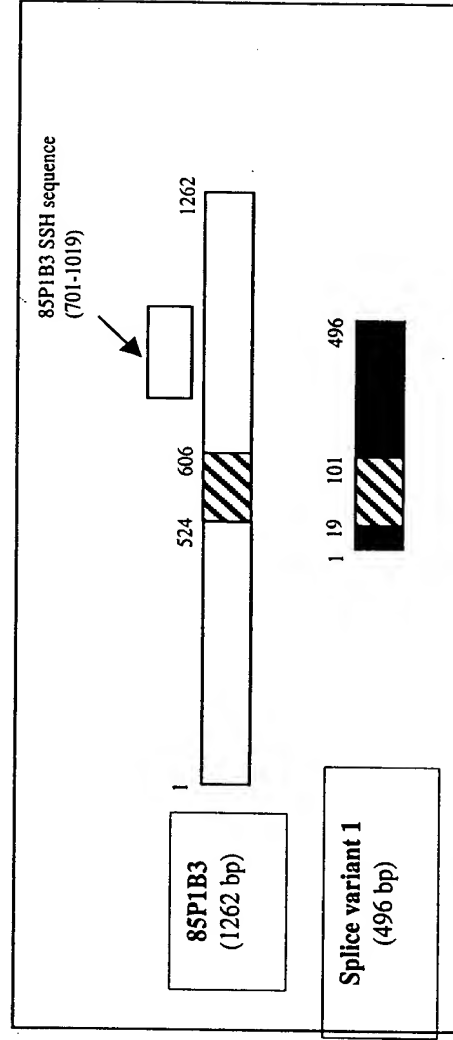


Figure 20

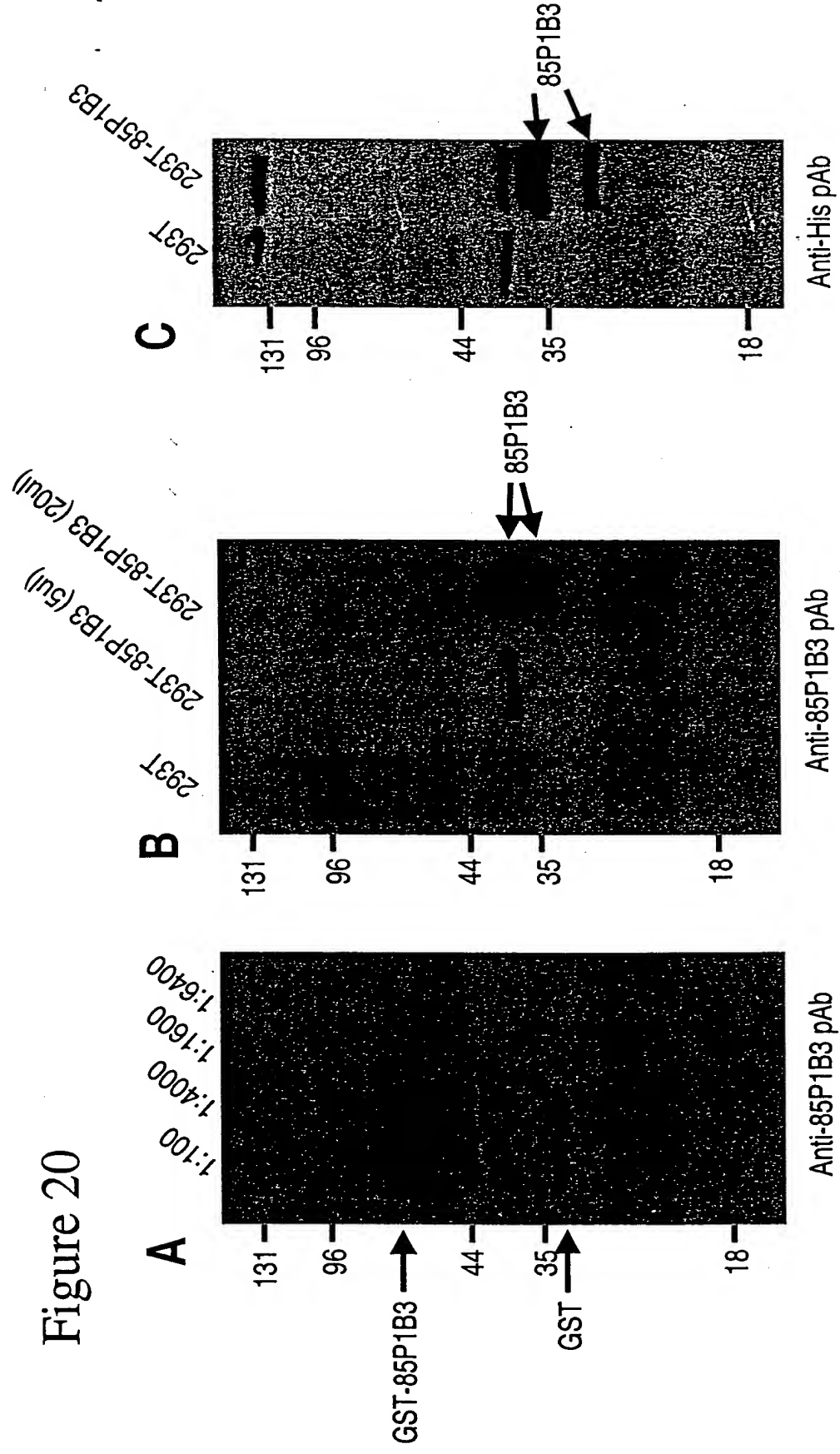


Fig. 21A

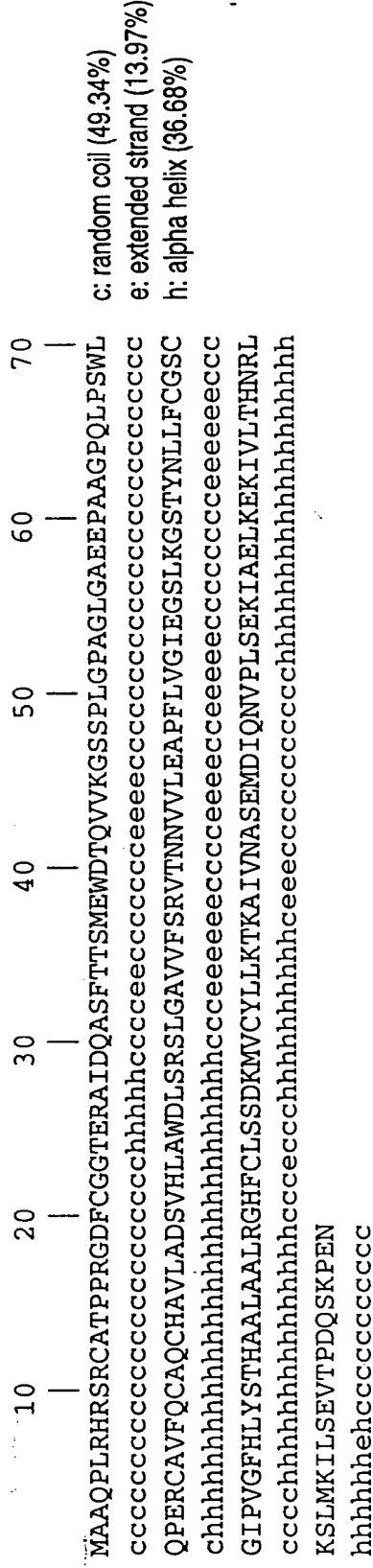


Fig. 21B

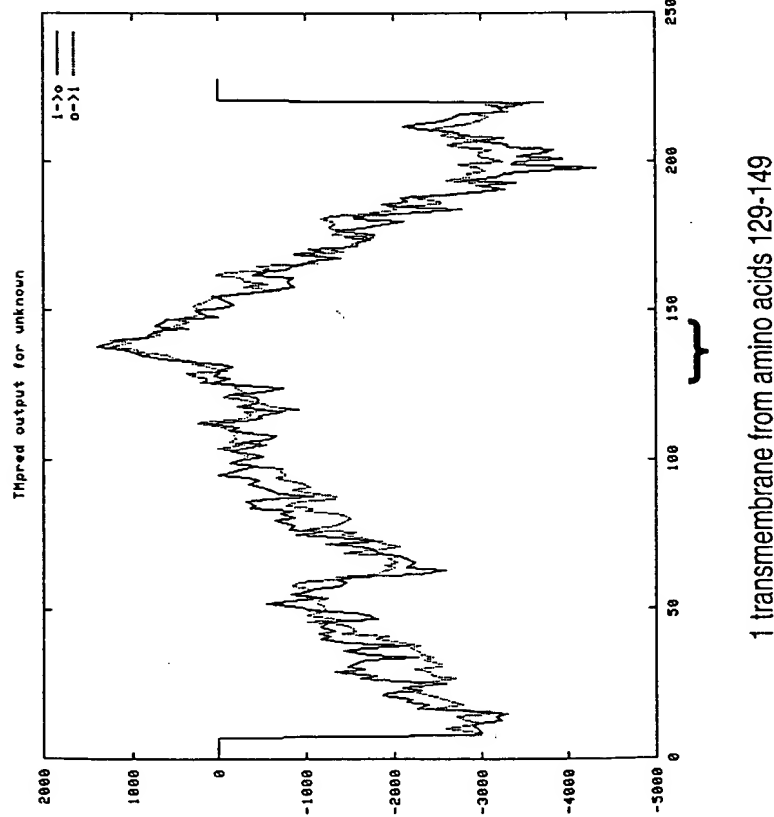


Fig. 21C

